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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/973,025

DATE: 11/30/2001
TIME: 16:06:22

Input Set : N:\Crf3\RULE60\09973025.txt
Output Set: N:\CRF3\11302001\I973025.raw

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SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: MAERTENS, GEERT
7 BOSMAN, FONS
8 DE MARTYNOFF, GUY
9 BUYSE, MARIE-ANGE
11 (ii) TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
12 PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
14 (iii) NUMBER OF SEQUENCES: 111
16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: NIXON & VANDERHYE P.C.
18 (B) STREET: 1100 NORTH GLEBE ROAD
19 (C) CITY: ARLINGTON
20 (D) STATE: VIRGINIA
21 (E) COUNTRY: U.S.A.
22 (F) ZIP: 22201-4714

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

30 (vi) CURRENT APPLICATION DATA:

31 (A) APPLICATION NUMBER: US/09/973,025
32 (B) FILING DATE: 10-Oct-2001
33 (C) CLASSIFICATION:

36 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US 08/612,973
38 (B) FILING DATE: 11-MAR-1996

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: BYRNE, THOMAS E.
43 (B) REGISTRATION NUMBER: 32,205
44 (C) REFERENCE/DOCKET NUMBER: 1487-10

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: (703) 816-4000
48 (B) TELEFAX: (703) 816-4100

52 (2) INFORMATION FOR SEQ ID NO: 1:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 21 base pairs
56 (B) TYPE: nucleic acid
57 (C) STRANDEDNESS: single
58 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: cDNA

62 (iii) HYPOTHETICAL: NO

64 (iv) ANTI-SENSE: NO

69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

71 GGCATGCAAG CTTAATTAAT T

73 (2) INFORMATION FOR SEQ ID NO: 2:

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75 (i) SEQUENCE CHARACTERISTICS:
 76 (A) LENGTH: 68 base pairs
 77 (B) TYPE: nucleic acid
 78 (C) STRANDEDNESS: single
 79 (D) TOPOLOGY: linear
 81 (ii) MOLECULE TYPE: cDNA
 83 (iii) HYPOTHETICAL: NO
 C--> 85 (iv) ANTI-SENSE: NO
 89 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 91 CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT 60
 93 TAACTGCA 68
 95 (2) INFORMATION FOR SEQ ID NO: 3:
 97 (i) SEQUENCE CHARACTERISTICS:
 98 (A) LENGTH: 642 base pairs
 99 (B) TYPE: nucleic acid
 100 (C) STRANDEDNESS: single
 101 (D) TOPOLOGY: linear
 103 (ii) MOLECULE TYPE: cDNA
 105 (iii) HYPOTHETICAL: NO
 C--> 107 (iv) ANTI-SENSE: NO
 110 (ix) FEATURE:
 111 (A) NAME/KEY: CDS
 112 (B) LOCATION: 1..639
 114 (ix) FEATURE:
 115 (A) NAME/KEY: mat_peptide
 116 (B) LOCATION: 1..636
 119 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 121 ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT 48
 122 Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys
 123 1 5 10 15
 125 CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG 96
 126 Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met
 127 20 25 30
 129 TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA 144
 130 Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala
 131 35 40 45
 133 GCG GAC ATC ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG 192
 134 Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu
 135 50 55 60
 137 AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT 240
 138 Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala
 139 65 70 75 80
 141 AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG 288
 142 Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu
 143 85 90 95
 145 CTC GTT GGG GCG GCT GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC 336
 146 Leu Val Gly Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu
 147 100 105 110
 149 TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC 384

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150	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	
151		115			120							125					
153	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC	432
154	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	
155						130		135				140					
157	ATA	ACA	GGT	CAC	CGT	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	480
158	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	
159	145					150				155				160			
161	ACA	ACG	GCC	CTG	GTG	GTA	TCG	CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	528
162	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	
163						165			170			175					
165	GTG	GAC	ATG	GTG	GCG	GGG	GCC	CAT	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	576
166	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	
167						180			185			190					
169	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	GTG	ATG	CTA	624
170	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile	Val	Met	Leu	
171					195				200			205					
173	CTC	TTT	GCT	CTC	TAATAG											642	
174	Leu	Phe	Ala	Leu													
175		210															
178	(2)	INFORMATION FOR SEQ ID NO: 4:															
180		(i)	SEQUENCE CHARACTERISTICS:														
181			(A)	LENGTH:	212	amino acids											
182			(B)	TYPE:	amino acid												
183			(D)	TOPOLOGY:	linear												
185		(ii)	MOLECULE TYPE:	protein													
187		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 4:														
189	Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	
190	1				5				10			15					
192	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	
193					20				25			30					
195	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	
196					35				40			45					
198	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	
199					50				55			60					
201	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	
202					65				70			75			80		
204	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu		
205						85				90			95				
207	Leu	Val	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu		
208						100			105			110					
210	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	
211					115				120			125					
213	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	
214					130				135			140					
216	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	
217					145				150			155			160		
219	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	
220						165			170			175					

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222 Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala
223 180 185 190
225 Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu
226 195 200 205
228 Leu Phe Ala Leu
229 210

232 (2) INFORMATION FOR SEQ ID NO: 5:

234 (i) SEQUENCE CHARACTERISTICS:
235 (A) LENGTH: 795 base pairs
236 (B) TYPE: nucleic acid
237 (C) STRANDEDNESS: single
238 (D) TOPOLOGY: linear

240 (ii) MOLECULE TYPE: cDNA

242 (iii) HYPOTHETICAL: NO

C--> 244 (iv) ANTI-SENSE: NO

247 (ix) FEATURE:

248 (A) NAME/KEY: CDS

249 (B) LOCATION: 1..792

251 (ix) FEATURE:

252 (A) NAME/KEY: mat_peptide

253 (B) LOCATION: 1..789

256 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

258 ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
259 Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
260 1 5 10 15	
262 GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
263 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
264 20 25 30	
266 GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
267 Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
268 35 40 45	
270 ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
271 Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
272 50 55 60	
274 CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
275 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
276 65 70 75 80	
278 TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
279 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
280 85 90 95	
282 TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
283 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
284 100 105 110	
286 GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
287 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
288 115 120 125	
290 CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
291 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
292 130 135 140	

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294	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	480
295	Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	
296	145				150					155					160		
298	GGG	GAC	CTC	TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	ATC	528
299	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	
300					165					170					175		
302	TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	576
303	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	
304					180					185					190		
306	CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	624
307	Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	
308					195					200					205		
310	TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG	GTA	TCG	CAG	CTG	CTC	CGG	ATC	CCA	672
311	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	
312					210					215					220		
314	CAA	GCT	GTC	GTG	GAC	ATG	GTG	GCG	GGG	GCC	CAT	TGG	GGA	GTC	CTG	GCG	720
315	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	
316					225					230					235		
318	GGT	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	768
319	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile	
320					245					250					255		
322	GTG	ATG	CTA	CTC	TTT	GCT	CCC	TAATAG									795
323	Val	Met	Leu	Leu	Phe	Ala	Pro										
324					260												
327	(2)	INFORMATION FOR SEQ ID NO: 6:															
329		(i)	SEQUENCE CHARACTERISTICS:														
330			(A)	LENGTH: 263 amino acids													
331			(B)	TYPE: amino acid													
332			(D)	TOPOLOGY: linear													
334		(ii)	MOLECULE TYPE: protein														
336		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 6:														
338	Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
339	1				5				10						15		
341	Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
342					20				25						30		
344	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
345					35				40						45		
347	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
348					50				55						60		
350	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
351	65				70					75					80		
353	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
354					85				90						95		
356	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
357					100				105						110		
359	Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	
360					115				120						125		
362	Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	
363					130				135						140		

VERIFICATION SUMMARY
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Input Set : N:\Crf3\RULE60\09973025.txt
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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:64 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:107 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:244 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:402 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:470 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:539 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:590 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
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L:954 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:974 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:994 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1014 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:1281 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:1684 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:2308 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:3101 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3447 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3663 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:4727 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:4930 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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